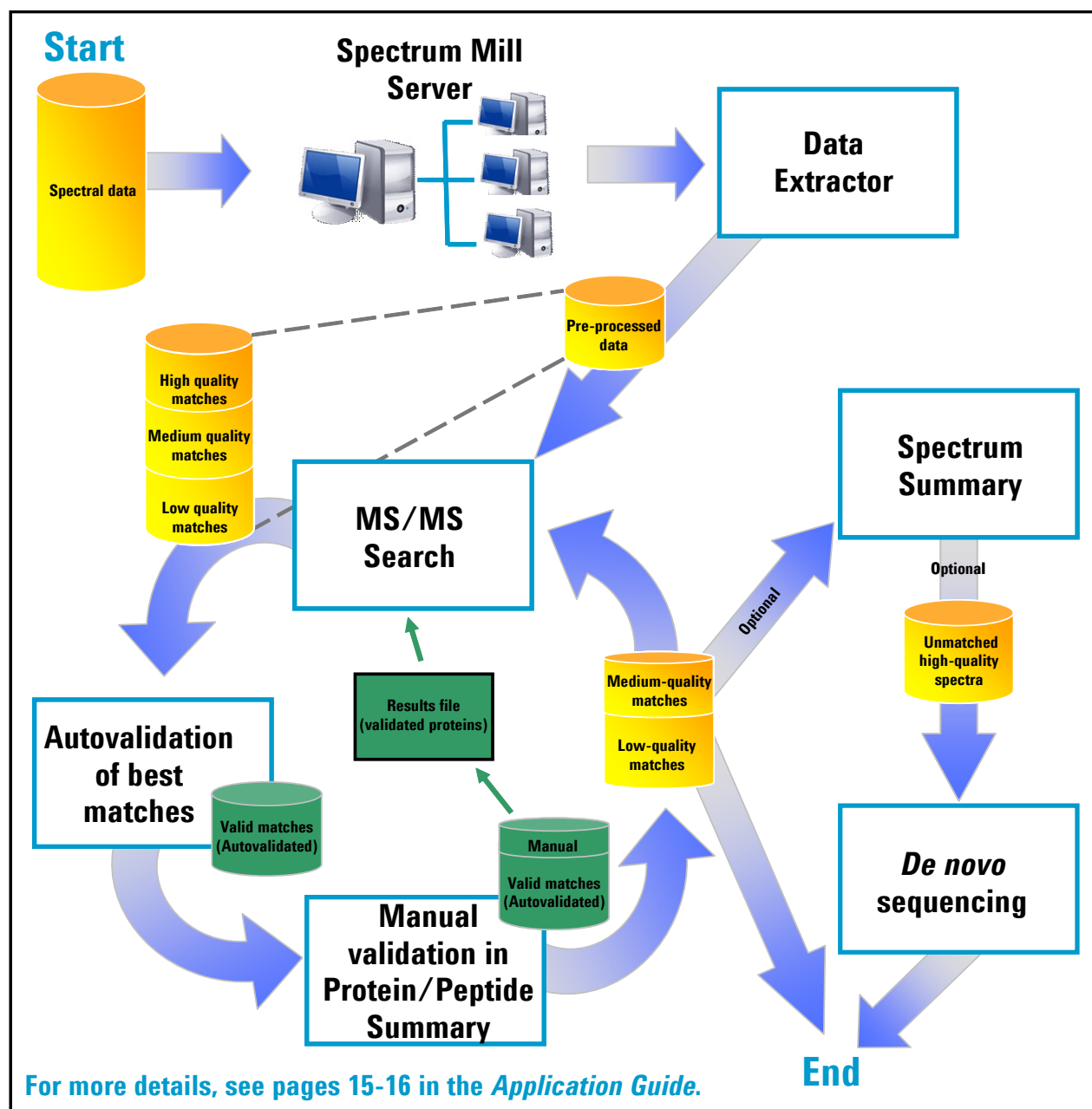


## Spectrum Mill MS Proteomics Workbench Quick Reference



**Figure 1** Summary of iterative processing for MS/MS data



Agilent Technologies



## Modes for Protein/Peptide Summary

If you want to:	And you want results organized by:	Then use this mode:	Example application
Validate results	Peptides	Peptide	Manual review and validation of MS/MS search results, organized by peptide
	Proteins, then peptides	Protein Summary Details	Manual review and validation of MS/MS search results, organized by protein
	Samples, then proteins, then peptides	Protein-Sample Centric Rows Details	Manual review and validation of MS/MS search results, organized by sample
Summarize results by proteins	Proteins only	Protein Summary	List of all proteins identified in the data
	Proteins, then samples	Protein-Protein Comparison Columns	Compare two or more samples, each of which may contain multiple fractions. Each sample (with all fractions) is organized in a separate directory.
	Proteins, then redundant hits	Protein-Protein Comparison Redundant	Same as immediately above, with additional detail on isoforms of proteins
	Proteins, then peptides	Protein Summary Details	View proteins, with supporting peptide details
Summarize results by samples	Samples, then proteins	Protein-Sample Centric Rows	View proteins from multiple 2D gel spots organized in a single directory
	Samples, then proteins, then peptides	Protein-Sample Centric Rows Details	Same as immediately above, with supporting peptide details
Summarize results by peptides	Peptides only	Peptide	List of all peptides identified in the data
	Peptides, then samples	Protein-Peptide Distribution Columns	Method development (evaluation of 2D LC/MS/MS or other fractionation scheme)
	Peptides, then samples	Protein-Peptide Comparison Columns	Evaluation of fractionation scheme (provides more information and easier export to Excel)
View a list of proteins identified via a single peptide	Peptides only	Protein-Single Peptide ID	Examination of results where a single peptide was used to generate a protein identification

For more details, see Chapter 2 in the *Application Guide*.

